



SEQUENCE LISTING

<110> Morrow, Casey D.
Porter, Donna C.
Ansardi, David C.

<120> ENCAPSIDATED RECOMBINANT POLIOVIRUS
NUCLEIC ACID AND METHODS OF MAKING AND USING SAME

<130> 532572000104

<140> 09/756,551

<141> 2001-01-08

<150> 09/376,184

<151> 1999-08-17

<150> 08/987,867

<151> 1997-12-09

<150> 08/389,459

<151> 1995-02-15

<150> 08/087,009

<151> 1993-07-01

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<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

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tattagtaga tctg

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<223> oligonucleotide

<400> 2

tacagatgta ctaa

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<210> 3

<211> 845

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<213> Artificial Sequence

<220>

<221> CDS

<222> (20)...(845)

<223> gag sequence

<400> 3

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Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly	
1 5 10	
caa atg gta cat cag gcc ata tca cct aga act tta aat gca tgg gta	100
Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val	
15 20 25	
aaa gta gta gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt	148
Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe	
30 35 40	
tca gca tta tca gaa gga gcc acc cca caa gat tta aac acc atg cta	196
Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu	
45 50 55	
aac aca gtg ggg gga cat caa gca gcc atg caa atg tta aaa gag acc	244
Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr	
60 65 70 75	
atc aat gag gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca	292
Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala	
80 85 90	
ggg cct att gca cca ggc cag atg aga gaa cca agg gga agt gac ata	340
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile	
95 100 105	
gca gga act act agt acc ctt cag gaa caa ata gga tgg atg aca aat	388
Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn	
110 115 120	
aat cca cct atc cca gta gga gaa att tat aaa aga tgg ata atc ctg	436
Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu	
125 130 135	
gga tta aat aaa ata gta aga atg tat agc cct acc agc att ctg gac	484
Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp	
140 145 150 155	
ata aga caa gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc	532
Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe	
160 165 170	
tat aaa act cta aga gcc gag caa gct tca cag gag gta aaa aat tgg	580
Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp	
175 180 185	
atg aca gaa acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act	628
Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr	
190 195 200	
att tta aaa gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca	676
Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr	
205 210 215	
gca tgt cag gga gta gga gga ccc gcg cat aag gca aga gtt ttg gct	724
Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala	
220 225 230 235	
gaa gca atg agc caa gta aca aat tca gct acc ata atg atg cag aga	772

Glu Ala Met Ser Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg
 240 245 250

ggc aat ttt agg aac caa aga aag att gtt aag tgt ttc aat tgt ggc 820
 Gly Asn Phe Arg Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly
 255 260 265

aaa gaa ggg cac aca gcc aga aag t 845
 Lys Glu Gly His Thr Ala Arg Lys
 270 275

<210> 4

<211> 275

<212> PRT

<213> Artificial Sequence

<220>

<223> Corresponding gag protein

<400> 4

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
 1 5 10 15
 Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
 20 25 30
 Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
 35 40 45
 Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
 50 55 60
 His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
 65 70 75 80
 Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
 85 90 95
 Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
 100 105 110
 Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
 115 120 125
 Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
 130 135 140
 Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
 145 150 155 160
 Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
 165 170 175
 Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
 180 185 190
 Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
 195 200 205
 Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
 210 215 220
 Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln
 225 230 235 240
 Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn
 245 250 255
 Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr
 260 265 270
 Ala Arg Lys
 275

<210> 5

<211> 948

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (4)...(946)

<223> pol sequence

<400> 5

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Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile		
1				5				10						15		
tgt	aca	gag	atg	gaa	aag	gaa	ggg	aaa	att	tca	aaa	att	ggg	cct	gaa	96
Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	
				20				25						30		
aat	cca	tac	aat	act	cca	gta	ttt	gcc	ata	aag	aaa	aaa	gac	agt	act	144
Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	
			35					40					45			
aaa	tgg	aga	aaa	tta	gta	gat	ttc	aga	gaa	ctt	aat	aag	aga	act	caa	192
Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	
		50					55						60			
gac	ttc	tgg	gaa	gtt	caa	tta	gga	ata	cca	cat	ccc	gca	ggg	tta	aaa	240
Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	
	65					70					75					
aag	aaa	aaa	tca	gta	aca	gta	ctg	gat	gtg	ggg	gat	gca	tat	ttt	tca	288
Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	
	80				85				90						95	
gtt	ccc	tta	gat	gaa	gac	ttc	agg	aag	tat	act	gca	ttt	acc	ata	cct	336
Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	
				100				105						110		
agt	ata	aac	aat	gag	aca	cca	ggg	att	aga	tat	cag	tac	aat	gtg	ctt	384
Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	
		115						120					125			
cca	cag	gga	tgg	aaa	gga	tca	cca	gca	ata	ttc	caa	agt	agc	atg	aca	432
Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	
		130					135					140				
aaa	atc	tta	gag	cct	ttt	aga	aaa	caa	aat	cca	gac	ata	gtt	atc	tat	480
Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	
	145					150					155					
caa	tac	atg	gat	gat	ttg	tat	gta	gga	tct	gac	tta	gaa	ata	ggg	cag	528
Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	
	160				165				170					175		
cat	aga	aca	aaa	ata	gag	gag	ctg	aga	caa	cat	ctg	ttg	agg	tgg	gga	576
His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	
			180					185					190			
ctt	acc	aca	cca	gac	aaa	aaa	cat	cag	aaa	gaa	cct	cca	ttc	ctt	tgg	624
Leu	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	
			195					200					205			
atg	ggg	tat	gaa	ctc	cat	cct	gat	aaa	tgg	aca	gta	cag	cct	ata	gtg	672
Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	
		210					215					220				

ctg	cca	gaa	aaa	gac	agc	tgg	act	gtc	aat	gac	ata	cag	aag	tta	gtg	720
Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	
	225					230					235					
ggg	aaa	ttg	aat	tgg	gca	agt	cag	att	tac	cca	ggg	att	aaa	gta	agg	768
Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Pro	Gly	Ile	Lys	Val	Arg	
240					245					250					255	
caa	tta	tgt	aaa	ctc	ctt	aga	gga	acc	aaa	gca	cta	aca	gaa	gta	ata	816
Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	Val	Ile	
			260						265					270		
cca	cta	aca	gaa	gaa	gca	gag	cta	gaa	ctg	gca	gaa	aac	aga	gag	att	864
Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	Glu	Ile	
			275					280					285			
cta	aaa	gaa	cca	gta	cat	gga	gtg	tat	tat	gac	cca	tca	aaa	gac	tta	912
Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp	Pro	Ser	Lys	Asp	Leu	
	290						295					300				
ata	gca	gaa	ata	cag	aag	cag	ggg	caa	ggc	ctc	g	ag				948
Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Leu						
	305					310										

<210> 6

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> Corresponding pol protein

<400> 6

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Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	
		20						25					30			
Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	
	35					40						45				
Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	
50					55					60						
Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	
65				70					75					80		
Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	
			85					90					95			
Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	
	100							105					110			
Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	
	115					120						125				
Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	
130					135					140						
Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	
145				150					155					160		
Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	
			165					170					175			
Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Leu	
		180					185					190				
Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	
	195					200						205				
Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	
210					215						220					
Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	

225		230		235		240									
Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Pro	Gly	Ile	Lys	Val	Arg	Gln
				245					250					255	
Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	Val	Ile	Pro
			260					265					270		
Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	Glu	Ile	Leu
		275					280					285			
Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp	Pro	Ser	Lys	Asp	Leu	Ile
	290					295					300				
Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Leu						
305					310										

<210> 7
 <211> 1568
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (7)...(1565)
 <223> env sequence

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1 5 10	
gcc ccg gct ggt ttt gcg att cta aaa tgt aat aat aag acg ttc aat	96
Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn	
15 20 25 30	
gga aca gga cca tgt aca aat gtc agc aca gta caa tgt aca cat gga	144
Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly	
35 40 45	
att agg cca gta gta tca act caa ctg ctg tta aat ggc agt cta gca	192
Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala	
50 55 60	
gaa gaa gag gta gta att aga tct gtc aat ttc acg gac aat gct aaa	240
Glu Glu Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys	
65 70 75	
acc ata ata gta cag ctg aac aca tct gta gaa att aat tgt aca aga	288
Thr Ile Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg	
80 85 90	
ccc aac aac aat aca aga aaa aga atc cgt atc cag aga gga cca ggg	336
Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly	
95 100 105 110	
aga gca ttt gtt aca ata gga aaa ata gga aat atg aga caa gca cat	384
Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His	
115 120 125	
tgt aac att agt aga gca aaa tgg aat aac act tta aaa cag ata gat	432
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp	
130 135 140	
agc aaa tta aga gaa caa ttc gga aat aat aaa aca ata atc ttt aag	480
Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys	
145 150 155	

caa tcc tca gga ggg gac cca gaa att gta acg cac agt ttt aat tgt	528
Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys	
160 165 170	
gga ggg gaa ttt ttc tac tgt aat tca aca caa ctg ttt aat agt act	576
Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr	
175 180 185 190	
tgg ttt aat agt act tgg agt act gaa ggg tca aat aac act gaa gga	624
Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly	
195 200 205	
agt gac aca atc acc ctc cca tgc aga ata aaa caa att ata aac atg	672
Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met	
210 215 220	
tgg cag aaa gta gga aaa gca atg tat gcc cct ccc atc agt gga caa	720
Trp Gln Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln	
225 230 235	
att aga tgt tca tca aat att aca ggg ctg cta tta aca aga gat ggt	768
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly	
240 245 250	
ggt aat agc aac aat gag tcc gag atc ttc aga ctt gga gga gga gat	816
Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Gly Asp	
255 260 265 270	
atg agg gac aat tgg aga agt gaa tta tat aaa tat aaa gta gta aaa	864
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys	
275 280 285	
att gaa cca tta gga gta gca ccc acc aag gca aag aga aga gtg gtg	912
Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val	
290 295 300	
cag aga gaa aaa aga gca gtg gga ata gga gct ttg ttc ctt ggg ttc	960
Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe	
305 310 315	
ttg gga gca gca gga agc act atg ggc gca gcc tca atg acg ctg acg	1008
Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr	
320 325 330	
gta cag gcc aga caa tta ttg tct ggt ata gtg cag cag cag aac aat	1056
Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn	
335 340 345 350	
ttg ctg agg gct att gag gcg caa cag cat ctg ttg caa ctc aca gtc	1104
Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val	
355 360 365	
tgg ggc atc aag cag ctc caa gca aga atc cta gct gtg gaa aga tac	1152
Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr	
370 375 380	
cta aag gat caa cag ctc cta ggg att tgg ggt tgc tct gga aaa ctc	1200
Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu	
385 390 395	
att tgc acc act gct gtg cct tgg aat gct agt tgg agt aat aaa tct	1248
Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser	

400	405	410	
ctg gaa cag atc tgg aat cac acg acc tgg atg gag tgg gac aga gaa			1296
Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu			
415	420	425	430
att aac aat tac aca agc tta ata cac tcc tta att gaa gaa tcg caa			1344
Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln			
	435	440	445
aac cag caa gaa aag aat gaa caa gaa tta ttg gaa tta gat aaa tgg			1392
Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp			
	450	455	460
gca agt ttg tgg aat tgg ttt aac ata aca aat tgg ctg tgg tat ata			1440
Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile			
	465	470	475
aaa tta ttc ata atg ata gta gga ggc ttg gta ggt tta aga ata gtt			1488
Lys Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val			
	480	485	490
ttt gct gta ctt tct ata gtg aat aga gtt agg cag gga tat tca cca			1536
Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro			
495	500	505	510
tta tcg ttt cag acc cac ctc cca atc tc gag			1568
Leu Ser Phe Gln Thr His Leu Pro Ile			
	515		

<210> 8

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Corresponding env protein

<400> 8

Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro
1				5					10					15	
Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr
			20					25					30		
Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg
		35					40					45			
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
	50					55				60					
Glu	Val	Val	Ile	Arg	Ser	Val	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile
65				70					75					80	
Ile	Val	Gln	Leu	Asn	Thr	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn
			85					90					95		
Asn	Asn	Thr	Arg	Lys	Arg	Ile	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala
			100				105						110		
Phe	Val	Thr	Ile	Gly	Lys	Ile	Gly	Asn	Met	Arg	Gln	Ala	His	Cys	Asn
		115					120					125			
Ile	Ser	Arg	Ala	Lys	Trp	Asn	Asn	Thr	Leu	Lys	Gln	Ile	Asp	Ser	Lys
	130					135					140				
Leu	Arg	Glu	Gln	Phe	Gly	Asn	Asn	Lys	Thr	Ile	Ile	Phe	Lys	Gln	Ser
145				150					155					160	
Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Thr	His	Ser	Phe	Asn	Cys	Gly	Gly
			165					170						175	
Glu	Phe	Phe	Tyr	Cys	Asn	Ser	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Phe

			180					185					190				
Asn	Ser	Thr	Trp	Ser	Thr	Glu	Gly	Ser	Asn	Asn	Thr	Glu	Gly	Ser	Asp		
		195					200					205					
Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln		
	210					215					220						
Lys	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Ser	Gly	Gln	Ile	Arg		
225					230					235					240		
Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Asn		
			245					250					255				
Ser	Asn	Asn	Glu	Ser	Glu	Ile	Phe	Arg	Leu	Gly	Gly	Gly	Asp	Met	Arg		
		260					265					270					
Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu		
	275					280					285						
Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys	Arg	Arg	Val	Val	Gln	Arg		
	290					295					300						
Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Leu	Phe	Leu	Gly	Phe	Leu	Gly		
305					310					315					320		
Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Ala	Ser	Met	Thr	Leu	Thr	Val	Gln		
			325						330					335			
Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	Asn	Asn	Leu	Leu		
		340						345					350				
Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	Gln	Leu	Thr	Val	Trp	Gly		
	355						360					365					
Ile	Lys	Gln	Leu	Gln	Ala	Arg	Ile	Leu	Ala	Val	Glu	Arg	Tyr	Leu	Lys		
	370				375					380							
Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys		
385					390					395					400		
Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp	Ser	Asn	Lys	Ser	Leu	Glu		
			405						410					415			
Gln	Ile	Trp	Asn	His	Thr	Thr	Trp	Met	Glu	Trp	Asp	Arg	Glu	Ile	Asn		
		420						425					430				
Asn	Tyr	Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln		
	435						440					445					
Gln	Glu	Lys	Asn	Glu	Gln	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser		
	450					455					460						
Leu	Trp	Asn	Trp	Phe	Asn	Ile	Thr	Asn	Trp	Leu	Trp	Tyr	Ile	Lys	Leu		
465					470					475					480		
Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Val	Gly	Leu	Arg	Ile	Val	Phe	Ala		
			485						490					495			
Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr	Ser	Pro	Leu	Ser		
			500					505					510				
Phe	Gln	Thr	His	Leu	Pro	Ile											
		515															

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 <213> Artificial Sequence

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 <223> primer

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 caccctctc ctacgtaacc aaggatc

27

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 10
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 <210> 11
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 11
 ggagagagat gggagctcga gcgtc 25

 <210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 12
 gccccctat acgtattgtg 20

 <210> 13
 <211> 41
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 <220>
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 <210> 14
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 ctctatcctg agtccatat gtgtcgagca gtttttggtt tagcattg 48

 <210> 15
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> peptide

 <400> 15
 Thr Lys Asp Leu Thr Thr Tyr Gly
 1 5

 <210> 16
 <211> 2220

<212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(2203)
 <223> cDNA

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cga cca gca gac cag aca gtc aca gca gcc ttg aca aaa cgt tcc tgg      48
Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp
  1             5             10             15

aac tca agc act tct cca cag agg agg aca gag cag aca gca gag acc      96
Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr
             20             25             30

atg gag tct ccc tcg gcc cct ccc cac aga tgg tgc atc ccc tgg cag     144
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
             35             40             45

agg ctc ctg ctc aca gcc tca ctt cta acc ttc tgg aac ccg ccc acc     192
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
             50             55             60

act gcc aag ctc act att gaa tcc acg ccg ttc aat gtc gca gag ggg     240
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
             65             70             75             80

aag gag gtg ctt cta ctt gtc cac aat ctg ccc cag cat ctt ttt ggc     288
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
             85             90             95

tac agc tgg tac aaa ggt gaa aga gtg gat ggc aac cgt caa att ata     336
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
             100             105             110

gga tat gta ata gga act caa caa gct acc cca ggg ccc gca tac agt     384
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
             115             120             125

ggt cga gag ata ata tac ccc aat gca tcc ctg ctg atc cag aac atc     432
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
             130             135             140

atc cag aat gac aca gga ttc tac acc cta cac gtc ata aag tca gat     480
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
             145             150             155             160

ctt gtg aat gaa gaa gca act ggc cag ttc cgg gta tac ccg gag ctg     528
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
             165             170             175

ccc aag ccc tcc atc tcc agc aac aac tcc aaa ccc gtg gag gac aag     576
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
             180             185             190

gat gct gtg gcc ttc acc tgt gaa cct gag act cag gac gca acc tac     624
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
             195             200             205

ctg tgg tgg gta aac aat cag agc ctc ccg gtc agt ccc agg ctg cag     672
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln

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210	215	220	
ctg tcc aat ggc aac agg acc ctc act cta ttc aat gtc aca aga aat			720
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn			
225	230	235	240
gac aca gca agc tac aaa tgt gaa acc cag aac cca gtg agt gcc agg			768
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg			
	245	250	255
cgc agt gat tca gtc atc ctg aat gtc ctc tat ggc ccg gat gcc ccc			816
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro			
	260	265	270
acc att tcc cct cta aac aca tct tac aga tca ggg gaa aat ctg aac			864
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn			
	275	280	285
ctc tcc tgc cat gca gcc tct aac cca cct gca cag tac tct tgg ttt			912
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe			
	290	295	300
gtc aat ggg act ttc cag caa tcc acc caa gag ctc ttt atc ccc aac			960
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn			
305	310	315	320
atc act gtg aat aat agt gga tcc tat acg tgc caa gcc cat aac tca			1008
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser			
	325	330	335
gac act ggc ctc aat agg acc aca gtc acg acg atc aca gtc tat gca			1056
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala			
	340	345	350
gag cca ccc aaa ccc ttc atc acc agc aac aac tcc aac ccc gtg gag			1104
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
	355	360	365
gat gag gat gct gta gcc tta acc tgt gaa cct gag att cag aac aca			1152
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
	370	375	380
acc tac ctg tgg tgg gta aat aat cag agc ctc ccg gtc agt ccc agg			1200
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
385	390	395	400
ctg cag ctg tcc aat gac aac agg acc ctc act cta ctc agt gtc aca			1248
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
	405	410	415
agg aat gat gta gga ccc tat gag tgt gga atc cag aac gaa tta agt			1296
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
	420	425	430
gtt gac cac agc gac cca gtc atc ctg aat gtc ctc tat ggc cca gac			1344
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
	435	440	445
gac ccc acc att tcc ccc tca tac acc tat tac cgt cca ggg gtg aac			1392
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
	450	455	460
ctc agc ctc tcc tgc cat gca gcc tct aac cca cct gca cag tat tct			1440

Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser		
465					470					475					480		
tgg	ctg	att	gat	ggg	aac	atc	cag	caa	cac	aca	caa	gag	ctc	ttt	atc		1488
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile		
				485					490					495			
tcc	aac	atc	act	gag	aag	aac	agc	gga	ctc	tat	acc	tgc	cag	gcc	aat		1536
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn		
			500					505					510				
aac	tca	gcc	agt	ggc	cac	agc	agg	act	aca	gtc	aag	aca	atc	aca	gtc		1584
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val		
		515					520					525					
tct	gcg	gag	ctg	ccc	aag	ccc	tcc	atc	tcc	agc	aac	aac	tcc	aaa	ccc		1632
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro		
		530				535					540						
gtg	gag	gac	aag	gat	gct	gtg	gcc	ttc	acc	tgt	gaa	cct	gag	gct	cag		1680
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln		
545					550					555					560		
aac	aca	acc	tac	ctg	tgg	tgg	gta	aat	ggt	cag	agc	ctc	cca	gtc	agt		1728
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser		
				565					570					575			
ccc	agg	ctg	cag	ctg	tcc	aat	ggc	aac	agg	acc	ctc	act	cta	ttc	aat		1776
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn		
			580					585					590				
gtc	aca	aga	aat	gac	gca	aga	gcc	tat	gta	tgt	gga	atc	cag	aac	tca		1824
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser		
		595					600					605					
gtg	agt	gca	aac	cgc	agt	gac	cca	gtc	acc	ctg	gat	gtc	ctc	tat	ggg		1872
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly		
		610				615					620						
ccg	gac	acc	ccc	atc	att	tcc	ccc	cca	gac	tcg	tct	tac	ctt	tcg	gga		1920
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly		
625					630					635					640		
gcg	aac	ctc	aac	ctc	tcc	tgc	cac	tcg	gcc	tct	aac	cca	tcc	ccg	cag		1968
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln		
				645					650					655			
tat	tct	tgg	cgt	atc	aat	ggg	ata	ccg	cag	caa	cac	aca	caa	gtt	ctc		2016
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu		
			660					665					670				
ttt	atc	gcc	aaa	atc	acg	cca	aat	aat	aac	ggg	acc	tat	gcc	tgt	ttt		2064
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe		
		675					680					685					
gtc	tct	aac	ttg	gct	act	ggc	cgc	aat	aat	tcc	ata	gtc	aag	agc	atc		2112
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile		
		690				695				700							
aca	gtc	tct	gca	tct	gga	act	tct	cct	ggt	ctc	tca	gct	ggg	gcc	act		2160
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Pro	Gly	Leu	Ser	Ala	Gly	Ala	Thr		
705					710					715					720		

gtc ggc atc atg att gga gtg ctg gtt ggg gtt gct ctg ata t 2203
 Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
 725 730

agcagccctg gtgtagt 2220

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<220>
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 Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr
 20 25 30
 Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
 35 40 45
 Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 50 55 60
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 65 70 75 80
 Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 85 90 95
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 100 105 110
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 115 120 125
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 130 135 140
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 145 150 155 160
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 165 170 175
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 180 185 190
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 195 200 205
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 210 215 220
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 225 230 235 240
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 245 250 255
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 260 265 270
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 275 280 285
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 290 295 300
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 305 310 315 320
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 325 330 335
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 340 345 350
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 355 360 365
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 370 375 380

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 385 390 395 400
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 405 410 415
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 420 425 430
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 435 440 445
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 450 455 460
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 465 470 475 480
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 485 490 495
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 500 505 510
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 515 520 525
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 530 535 540
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 545 550 555 560
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 565 570 575
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 580 585 590
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 595 600 605
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 610 615 620
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 625 630 635 640
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 645 650 655
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 660 665 670
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 675 680 685
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 690 695 700
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 705 710 715 720
 Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
 725 730

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<220>
 <223> primer

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41

<210> 19
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<220>

<223> primer

<400> 19

gatgaaccct cgagaccat tatg

24

<210> 20

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<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 20

ccaccaagta cgtaaccaca tatgg

25

<210> 21

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 21

gtgaggactg ctgg

14

<210> 22

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 22

caccactgcc ctcgagaagc tcactattg

29

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 23

caccactgcc ctcgagaagc tcactattg

29

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 24

Thr Thr Ala Lys Leu Thr

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5

<210> 25

<211> 5
<212> PRT
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<220>
<223> peptide

<400> 25
Met Gly Leu Glu Lys
1 5

<210> 26

<220>
<223> peptide

<400> 26
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